What is claimed is:

1. A nucleic acid having the formula R_A-R_B-R_C, wherein
   - R_A, R_B and R_C constitute component sequences consisting of nucleotide residues independently selected from the group of G, A, T and C or G, A, U and C, wherein
     G is Guanosinmonophosphate,
     A is Adenosinemonophosphate,
     T is Thymidinmonophosphate,
     U is Uridinmonophosphate and
     C is Cytidinmonophosphate;
   - R_A and R_C consist independently of 0 to 6000 nucleotide residues;
   - R_B consists of at least 50 nucleotide residues; and
   - the component sequence R_B is at least 80% identical to an aligned component sequence of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO: 27.

2. The nucleic acid of claim 1, wherein R_B consists of at least 100 nucleotide residues and is at least 85% identical to an aligned component sequence of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO: 27.

3. The nucleic acid of claim 1, wherein the nucleic acid sequence of R_B is the sequence given in SEQ ID NO: 7, SEQ ID NO: 9 or SEQ ID NO: 27.

4. The nucleic acid of claim 1, wherein R_A or R_C comprise one or more additional component sequences with a length of at least 50 nucleotide residues and at least 90% identical to an aligned component sequence of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO: 27.

5. The nucleic acid of any one of claims 1 to 4 comprising an open reading frame encoding a protein comprising a component sequence of at least 200 amino acids length being at least 85% identical to an aligned component sequence of SEQ ID NO: 10.

6. A method of selecting a plant which compared to a wild type plant is impaired in transcriptional gene silencing, comprising
   a) separately preparing RNA of a series of plants;
   b) probing said RNA preparations with a nucleic acid according to claim 1; and
   c) identifying a plant whose RNA hybridizes with said nucleic acid.

7. The method of claim 6, wherein process steps b) and c) comprise reverse transcription of the RNA and subsequent amplification of the generated DNA using oligonucleotide primers specific for SEQ ID NO: 1, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9 or SEQ ID NO: 27.

8. A method of producing DNA representing at least part of a gene necessary to maintain silencing of another gene in a cell or plant, comprising
   (a) mutagenizing wild type cells or plants by randomly inserting into their genomes a DNA tag with known sequence;
   (b) identifying mutants of said cells or plants which express RNA that is not expressed in wild type cells or plants;
   (c) cloning a piece of genomic DNA surrounding or close to the insertion site of the DNA tag;
   (d) screening a genomic library of wild type cells or plants with the piece of genomic DNA obtained in process step (c) or a part thereof;
   (e) identifying clones comprising at least part of the gene affected by the insertion of the DNA tag; and
   (f) further processing the clones obtained in step (e) using recombinant DNA techniques.

9. The method of claim 8, wherein plants are mutagenized using T-DNA, Ac/Ds or EN/I insertions, chemical or physical mutagenesis.

10. The method of claim 8, wherein mutants expressing RNA that is not expressed in wild type cells or plants are identified by reverse transcription of said RNA and subsequent amplification of the generated DNA using oligonucleotide primers specific for said DNA (RT-PCR).

11. The method according to claim 10, wherein pools of mutants are analyzed by RT-PCR.

12. The method according to claim 8, wherein the complete gene necessary to maintain silencing is produced.

13. A kit for the identification of plants impaired in transcriptional gene silencing comprising
    a) a nucleic acid according to claim 1 conveniently labeled to be used as a hybridization probe or
    b) an oligonucleotide primer for reverse transcription of RNA and an oligonucleotide primer specific for a nucleic acid according to claim 1.